

Figure 1: 121P1F1 SSH sequence of 254 nucleotides (SEQ ID: ____)

1 GATCACAGTC TTTGTATTT TCTACTTCTG CCTTTAGCTG TTCCCTTGG TCTCGAAGTG
61 AAGAAAGCTC TTTGCTAGC CTGGTTCGCT CTTCCGTTTC ACATCGGCCA ATTTAGCTT
121 TCTCAATGCT TTTCTGTAGG CTTGCATGCT TTTGACTTCC CTCAGACAAAC TGAGATTCCA
181 GAACCTCCAA CTTATGTTTC CTTGCATGAA GAGCTTACT TGGAAAAGCC CAATAATAAT
241 TAGAAGTTCC GATC

Figure 2: The cDNA and Amino Acid Sequence(s)

Figure 2A. The cDNA (SEQ ID. NO. : ____) and amino acid sequence (SEQ ID. NO. : ____) of

121P1F1. The start methionine is underlined. The open reading frame extends from nucleic acid 82-699 including the stop codon.

1 ccaaaaatcaaacgcgtccgggcctgtcccgccctctccccaagcgccggccggccagc
1 M S K K K G L S A E E K R
61 ggaagccctgcgcggcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTCTGAAACAAAGATGTATTCATTAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAATTGGC
114 R C E T E E R T R L A K E L S S L R D Q
421 CGATGTGAAACGGAAGAGCGAACCGAGCTAGCAAAAGAGCTTCTCAGTGGACCAA
134 R E Q L K A E V E K Y K D C D P Q V V E
481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
154 E I R Q A N K V A K E A A N R W T D N I
541 GAAATACGCCAAGCAAATAAAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATA
174 F A I K S W A K R K F G F E E N K I D R
601 TTCGCAATAAAATCTTGGGCCAAAAGAAAATTGGTTGAAGAAAATAAATTGATAGA
194 T F G I P E D F D Y I D *
661 ACTTTGGAAATTCCAGAAGACTTTGACTACATAGACTAAAtattccatgggtggtaagg
721 atgtacaagcttgtaaatgttaattttaactattatctaactaagtgtactgaattg
781 tcgtttgcctgttaactgtgtttatcatttattaaatgttaataaagtgtaaaatgcaaa
841 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :) and amino acid sequence (SEQ ID. NO. :) of 121P1F1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

1 ccaaaatcaaacgcgtccgggctgtcccgccctctcccaagcgccggccggccagc
1 M S K K K G L S A E E K R
61 ggaagccctgcgcggcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTCTGAAACAAAGATGTATTCATTAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q D
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGGAC
94 P G C C F H E I I K V S Y Y R K F W L G
361 CCTGGCTGCTGCTTCCATGAAATAATTAAAGTCTCCTATTATAGAAAATTCTGGCTGGC
114 A V A H A C N P S T L G G *
421 GCAGTGGCTCACGCCGTAAATCCCAGCACTTGGGAGGCTGAGgcgggagatcacgagg
481 tgactttccccacccccacatgaagtgcagatggagttgtctgagggaaagtcaaaagc
541 atgcaagcctacagaaaagcattgagaaagctaaaattggccatgtgaaacggaaagac
601 gaaccaggcttagcaaaagagcttcttcacttcgagaccaaaggaaacagctaaaggcag
661 aagtagaaaaatacaaagactgtgatccgcaagttgtgaaagaaatacgc当地
721 aagtagccaaaagaagactgctaaacagatggactgataacatattc当地
781 cccaaaagaaaaatttgggttgaagaaaataaaattgatagaactttgaaattcc
841 actttgactacatagactaaaatattccatgggtgaaggatgtacaagctgt
901 tgtaaaattttaactattactaactaagtgtactgaattgtcg
961 ttatcatttattaatgttaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaaaa

Figure 2C. The cDNA (SEQ ID. NO. :) and amino acid sequence (SEQ ID. NO. :) of 121P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

1 ccaaaaatcaaacgcgtccgggcctgtcccgccctctccccaaagcgccggccggccagc
61 ggaagccctgcgccccgcgcattgtcaaagaaaaaaggactgagtcagaagaaaagaga
121 actcgcatgtggaaatatttctgaaacaaaagatgtattcaattaaagacttggag
181 aagattgctcccaaagagaaaggcattactgctatgtcagtaaaagaagtcccaaagc
241 ttagttgatgtggatggttgactgtgagaggatcggaaacttctaattatttgggct
301 tttccaagtaaagctttcatgcaaggaaacataagttggaggttctggaatctcaggac
361 cctggctgctgcttccatgaaataattaaagtctcattatagaaaattctggctggc
421 gcagttggctcacgcctgtaatcccagcacttgggaggctgaggcgggcagatcacgagg
1 M K C K M E L S E G S Q K H
481 tgactttccccccacccacATGAAGTGCAAGATGGAGTTGTCTGAGGGAAGTCAAAGC
15 A S L Q K S I E K A K I G R C E T E E R
541 ATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAATTGGCCGATGTGAAACGGAAAGAGC
35 T R L A K E L S S L R D Q R E Q L K A E
601 GAACCAGGCTAGCAAAAGAGCTTCTTCACTCGAGACCAAAGGGAACAGCTAAAGGCAG
55 V E K Y K D C D P Q V V E E I R Q A N K
661 AAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATA
75 V A K E A A N R W T D N I F A I K S W A
721 AAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATATTGCAATAAAATCTGGG
95 K R K F G F E E N K I D R T F G I P E D
781 CCAAAAGAAAATTGGGTTGAGAAAATAAAATTGATAGAACTTTGGAATTCCAGAAG
115 F D Y I D *
841 ACTTTGACTACATAGACTAAatattccatggtggtgaaggatgtacaagcttgtaata
901 tgtaaattttaaactattatctaactaagtgtactgaattgtcggtgcctgtactgtg
961 tttatcattttatataatgttaataaaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaaa

Figure 2D. The cDNA (SEQ ID. NO. :) and amino acid sequence (SEQ ID. NO. :) of 121P1F1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.

1 ccaaaaatcaaacgcgtccgggactgtcccgccctctcccaagcgcggccggccagc
1 M S K K K G L S A E E K R
61 ggaagccctgcgcgcgcATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGAAATATTTCTGAAACAAAGATGTATTCATTAAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAAGTAAAGAAGTCCTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAAGTCAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T A K Q I K *
421 CGATGTGAAACGGCCAAGCAAATAAAGTAGccaaagaagctgctaacagatggactgata
481 acatattcgcaataaaatctggccaaaagaaaattgggttgaagaaaataaaattg
541 atagaacttttggattccagaagactttgactacatagactaaaatattccatgggt
601 gaaggatgtacaagcttgtaatatgtaaattttaactattatctaactaagtgtactg
661 aattgtcgttgcctgttaactgtgttatcatttatataatgttaataaagtgtaaaat
721 gcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Figure 2E. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid 82-654 including the stop codon.

1 cccaaaatcaaacgcgtccgggcctgtcccgcccccttcggggccggccagc
1 M S K K K G L S A E E K R
61 ggaagccccctgcgccccgcgcATGTCAAAGAAAAAGGACTGAGTCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTCTGAAACAAAAGATGTATTCATTAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAAGCTAAAATTGGC
114 R C E T E E R T R L A K E L S S L R D Q
421 CGATGTGAAACGGAAGAGCGAACCGAGCTAGCAAAAGAGCTTCTCACTTCGAGACCAA
134 R E Q L K A E V E K Y K D C D P Q V V E
481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
154 E I H N I F A I K S W A K R K F G F E E
541 GAAATACATAACATATTGCAATAAAATCTGGGCCAAAGAAAATTGGGTTGAAGAA
174 N K I D R T F G I P E D F D Y I D *
601 AATAAAATTGATAGAACCTTTGAAATTCCAGAAGACTTGAACATAGACTAAatatt
661 ccatgggtggtaaggatgtacaagctgtgaatatgtaaatttaactattatctaact
721 aagtgtactgaattgtcgttgcctgttaactgtgttatcatttattaaatgttaataa
781 aqtgtaaaaatqaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Figure 2F. The cDNA (SEQ ID. NO.:) and amino acid sequence (SEQ ID. NO.:) of 121P1F1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid 281-853 including the stop codon.

1 gttttctgtattgtatatgttagagcacattccagaactgctcagttcgagttacctaa
61 tggatcttcaactgtgtgccaatttagtcgattctgtgaaaacgccccggttctgcca
121 gggcaggaggctcgctgtgtgggtgtcgctgggtgttagggcgctgttgc
181 ttaaggacgcctgcactgaattaggcttcgtgggtcatgatcagttaa
1 M M E I F S E
241 aaagaaaaaggactgagtgcagaagaaaagagaactcgcATGATGGAAATATTTCTGA
8 T K D V F Q L K D L E K I A P K E K G I
301 AACAAAAGATGTATTCAATTAAAAGACTTGGAGAAGATTGCTCCAAAGAGAAAGGCAT
28 T A M S V K E V L Q S L V D D G M V D C
361 TACTGCTATGTCAGTAAAAGAAGTCCTCAAAGCTTAGTTGATGATGGTATGGTTGACTG
48 E R I G T S N Y Y W A F P S K A L H A R
421 TGAGAGGATCGGAACCTCTAATTATTGGGCTTCCAAGTAAAGCTCTTCATGCAAG
68 K H K L E V L E S Q L S E G S Q K H A S
481 GAAACATAAGTTGGAGGTTCTGGAATCTCAGTTGTCTGAGGGAAAGTC
441 AAAAGCATGCAAG
88 L Q K S I E K A K I G R C E T E E R T R
541 CCTACAGAAAAGCATTGAGAAAGCTAAATTGGCCGATGTGAAACGGAAGAGCGAAC
108 L A K E L S S L R D Q R E Q L K A E V E
601 GCTAGCAAAGAGCTTCTTCCTCGAGACCAAGGGAAACAGCTAAAGGCAGAAAGTAGA
128 K Y K D C D P Q V V E E I R Q A N K V A
661 AAAATACAAAGACTGTGATCCGCAAGTTGGAAGAAATACGCCAAGCAAATAAGTAGC
148 K E A A N R W T D N I F A I K S W A K R
721 CAAAGCAAGCTGCTAACAGATGGACTGATAACATATTGCAATAAAATCTGGCC
168 K F G F E E N K I D R T F G I P E D F D
781 AAAATTGGGTTGAAGAAAATAAATTGATAGAACCTTGGATTCCAGAAGACTTGA
188 Y I D *
841 CTACATAGACTAAatattccatgggtgaaggatgtacaagcttgc
901 tttaaaactattatctaactaagtgtactgaattgtcg
961 ttttattaatgttaataaaatgttaaaatgc
1021 aaaggcaggatgataaccatatcccccc
1081 ccatctcagtcaaagg
1141 tccaagcttacgtacgcgtgc
1201 aagtt

Figure 3:

Figure 3A. Amino acid sequence of 121P1F1 (SEQ ID. NO. :____). The 121P1F1 protein has 205 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPIKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
121 TRLAKELSSL RDQREQLKAЕ VEKYKDCDPQ VVEEIRQANK VAKEAANRWT DNIFAIKSWA
181 KRKFGFEENK IDRTFGIPED FDYID

Figure 3B. Amino acid sequence of 121P1F1 splice variant 1A (SEQ ID. NO. :____). The 121P1F1 splice variant 1A protein has 126 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPIKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQDPGCCFHE IIKVSYYRKF WLGAVALHACN
121 PSTLGG

Figure 3C. Amino acid sequence of 121P1F1 splice variant 1B (SEQ ID. NO. :____). The 121P1F1 splice variant 1B protein has 119 amino acids.

1 MKCKMELSEG SQKHASLQKS IEKAKIGRCE TEERTRLAKE LSSLRDQREQ LKAEVEKYKD
61 CDPQVVEEIR QANKVAKEAA NRWTDNIFAI KSWAKRKFGF EENKIDRTFG IPEDFDYID

Figure 3D. Amino acid sequence of 121P1F1 splice variant 2 (SEQ ID. NO. :____). The 121P1F1 splice variant 2 protein has 122 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPIKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETAKQ
121 IK

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO. : ____). The 121P1F1 splice variant 3 protein has 190 amino acids.

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1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER
121 TRLAKELSSL RDQREQQLKAE VEKYKDCDPQ VVEEIHNIKA IKSWAKRKFG FEENKIDRTF
181 GIPEDFDYID
```

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO. : ____). The 121P1F1 splice variant 4 protein has 190 amino acids.

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1 MMEIFSETKD VFQLKDLEKI APKEKGITAM SVKEVLQSLV DDGMVDCERI GTSNYYWAFP
61 SKALHARKHK LEVLESQSLSE GSQKHASLQK SIEKAKIGRC ETEERTRLAK ELSSLRDQRE
121 QLKAEVEKYK DCDPQVVEEI RQANKVAKEA ANRWTDNIFA IKSWAKRKFG FEENKIDRTF
181 GIPEDFDYID
```

Figure 4A

Amino Acid Alignments.

Alignment of 121P1F1 protein and its variants.

A) CLUSTAL W alignment of 121P1F1 and variants 1-3.

121P1F01	-----MSKKKGLSAEKRTRMMEIFSETKDVQLKDEKIAPIKEKGITAMSVKE
sv1A	-----MSKKKGLSAEKRTRMMEIFSETKDVQLKDEKIAPIKEKGITAMSVKE
sv1B	-----MKCKMELSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
sv-2	-----MSKKKGLSAEKRTRMMEIFSETKDVQLKDEKIAPIKEKGITAMSVKE
sv-3	-----MSKKKGLSAEKRTRMMEIFSETKDVQLKDEKIAPIKEKGITAMSVKE
121P1F01	VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLEGSQK-HASLQKS-I
sv1A	VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQDP-GCCF-HEIIKVSVYY
sv1B	QLKAEVEK-YKDCDPQVVEEIRQANKVAKEAANRWTNDNIFAIKSWAKRKGFEENKID--
sv-2	VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLEGSQK-HASLQKS-I
sv-3	VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLEGSQK-HASLQKS-I
121P1F01	EKAKIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAAN
sv1A	RKFWLGAVALHACNPSTLGG-----
sv1B	RTFGIPEDFDYID-----
sv-2	EKAKIGRCETAKQIK-----
sv-3	EKAKIGRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIHNIFAIKSWAKR
121P1F01	RWTNDNIFAIKSWAKRKGFEENKIDRTFGIPEDFDYID
sv1A	-----
sv1B	-----
sv-2	-----
sv-3	KFGFEENKIDRTFGIPEDFDYID-----

Figure 4B

Clustal alignment of 121P1F1 and variants 1A and 4

1	15	16	30	31	45	46	60	61	75	76	90	
1 121P1F01	MSKKKGLSAEKRTR	MMEIFSETKDVQLK	DLEKIAPIKEKGITAM	SVKEVLQLSLVDDGMV	DCERIGTSNYYWAFP	SKALHARKHKLEVLE						
2 sv-4	-----	MMEIFSETKDVQLK	DLEKIAPIKEKGITAM	SVKEVLQLSLVDDGMV	DCERIGTSNYYWAFP	SKALHARKHKLEVLE						
3 sv-1A	MSKKKGLSAEKRTR	MMEIFSETKDVQLK	DLEKIAPIKEKGITAM	SVKEVLQLSLVDDGMV	DCERIGTSNYYWAFP	SKALHARKHKLEVLE						
-												
1 121P1F01	91	105	106	120	121	135	136	150	151	165	166	180
2 sv-4	SQLSEGSQKHASLQK	SIEKAKIGRCETEER	TRLAKELSSLRDQRE	QLKAEVEKYKDCDPQ	VVEEIRQANKVAKEA	ANRWTNDNIFAIKSWA						
3 sv-1A	SQLSEGSQKHASLQK	SIEKAKIGRCETEER	TRLAKELSSLRDQRE	QLKAEVEKYKDCDPQ	VVEEIRQANKVAKEA	ANRWTNDNIFAIKSWA						
-												
1 121P1F01	181	195	196	210	211							
2 sv-4	KRKFGFEENKIDRTF	GIPEDFDYID	205									
3 sv-1A	KRKFGFEENKIDRTF	GIPEDFDYID	190									
-				126								

Figure 4C

C) Alignment with human GAJ

Identities = 205/205 (100%), Positives = 205/205 (100%)

121P1: 1 MSKKKGLSAAEKRTRMMEIFSETKDVFQLKDLLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
MSKKKGLSAAEKRTRMMEIFSETKDVFQLKDLLEKIAPKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1 MSKKKGLSAAEKRTRMMEIFSETKDVFQLKDLLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQLKHSIEKAKIGRCETEER 120
DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQLKHSIEKAKIGRCETEER
Sbjct: 61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQLKHSIEKAKIGRCETEER 120

121P1: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKEEANRWTDNIFAISWA 180
TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKEEANRWTDNIFAISWA
Sbjct: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKEEANRWTDNIFAISWA 180

121P1: 181 KRKFGFEENKIDRTFGIPEDFDYID 205
KRKFGFEENKIDRTFGIPEDFDYID
Sbjct: 181 KRKFGFEENKIDRTFGIPEDFDYID 205

Figure 4D

D) Alignment with closest mouse homolog, a hypothetical 24.2 KDa protein.

Identities = 183/205 (89%), Positives = 193/205 (93%)

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121P1: 1  MSKKGLSAAEKRTRMMEIFSETKDVQLKDLKEIAPKEKGITAMSVKEVLQSLVDDGMV 60
          MSKK+GLS  EEKRTRMMEIF  ETKDVQLKDLK+APKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1  MSKKRGLSGEEKRTRMMEIFFETKDVQLKDLKEIAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61  DCERIGTSNYYWAFPSKALHARKHLEVLESQLEGSQKHASLQKSIEKAKIGRCETEER 120
          DCERIGTSNYYWAFPSKALHARK  KLE L SQLSEGSQKHA LQKSIEKA++GR ETEER
Sbjct: 61  DCERIGTSNYYWAFPSKALHARKRKLLEALNSQLEGSQKHA DLQKSIEKARVGRQETEER 120

121P1: 121  TRLAKELSSLRDQRQLKAEVEKYKDCDPQVVEIRQANKVAKEAANRWTDNIFAISWA 180
          LAKEL S RDQR+QLKAEVEKY++CDPQVVEIR+ANKVAKEAANRWTDNIFAISWA
Sbjct: 121  AMLAKELFSFRDQRQQLKAEVEKYRECDPQVVEIREANKVAKEAANRWTDNIFAISWA 180

121P1: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
          KRKFGFEE+KID+ FGIPEDFDYID
Sbjct: 181  KRKFGFEESKIDKNFGIPEDFDYID 205
```

Figure 4E

E. >gi|1175412|sp|Q09739|YA53_SCHPO HYPOTHETICAL 24.2 KD PROTEIN C13A11.03
IN CHROMOSOME I
gi|7490680|pir||T37610 hypothetical coiled-coil protein - fission yeast
(Schizosaccharomyces pombe)
gi|984224|emb|CAA90804.1| (Z54096) hypothetical coiled-coil protein
[Schizosaccharomyces pombe]
Length = 210

Score = 121 bits (305), Expect = 5e-27
Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps = 6/202 (2%)

Query: 5 KGLSAEEKRTRMMEIFSETKDVQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64
KGLS EKR R+ IF ++KD FQLK++EK+ K K I +VK+VLQSLVDD +V E+
Sbjct: 4 KGLSLAEKRRRLEAIFHDSKDFQLKEVEKLGSK-KQIVLQTVKDVLQSLVDDNIVKTEK 62

Query: 65 IGTSNYYWAFPSKALHARKHKLEVLESQQLSEGSQKHASLQKSIEKAKIGR---CETEER 120
IGTSNYYW+FPS A +R+ L L++QL + QK +L ++I K R E +
Sbjct: 63 IGT SNYYW FPS DAKRSRESV LGS LQ A QL DDL K Q K S K T L D E N I S F E K S K R D N E G T E N D A N 122

Query: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
+ L + + + LK ++ C+P+ E + K EAAN WTD I + ++
Sbjct: 123 QYTLELLHAKESELKLLKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC 182

Query: 181 KRKFGFEENKIDRTFGIPEDFD 202
R G + N+I IPED D
Sbjct: 183 -RDMGADTNQIREYCSIPEDLD 203

Figure 5A
121P1F1 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

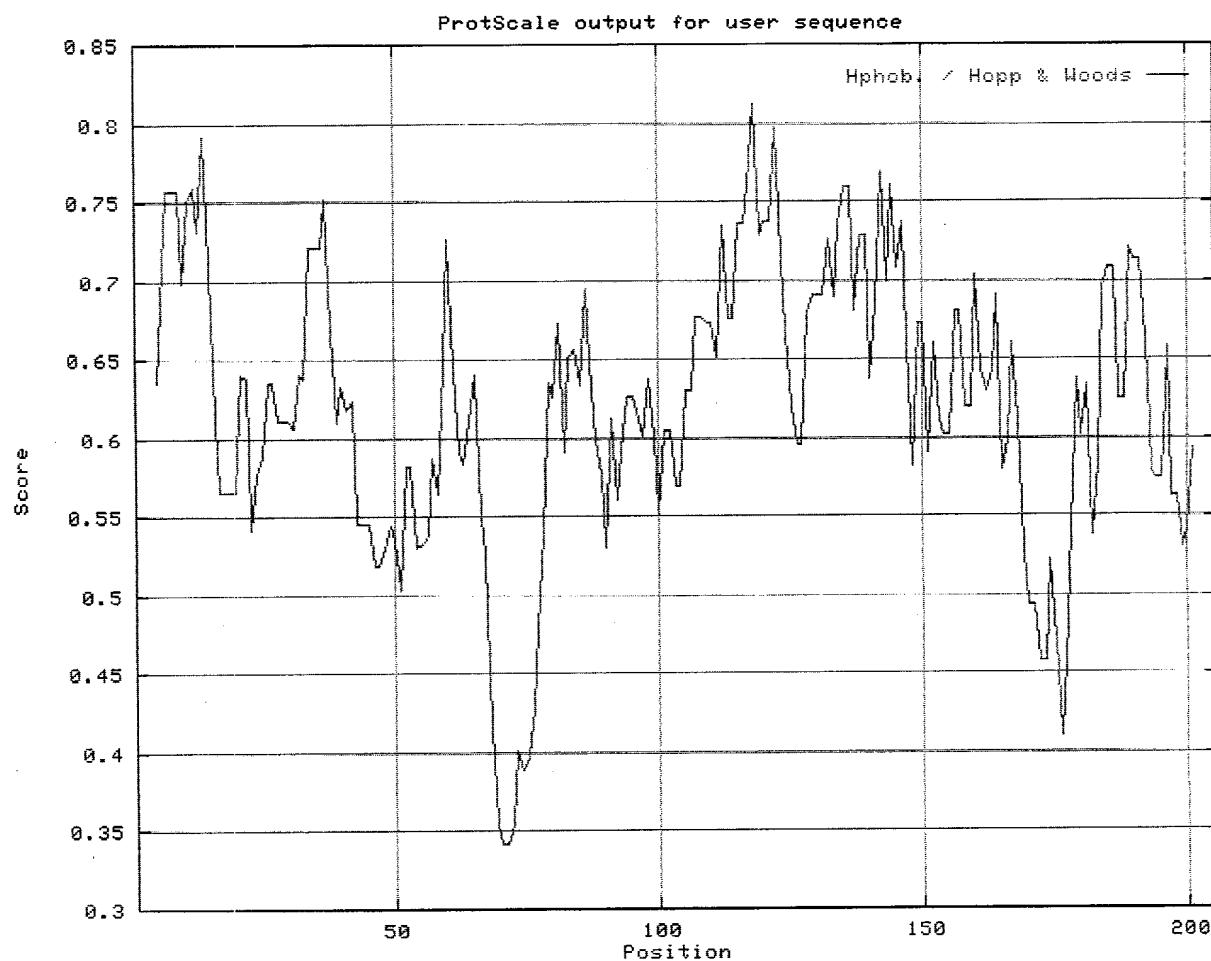


Figure 5B

121P1F1 variant 1a Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

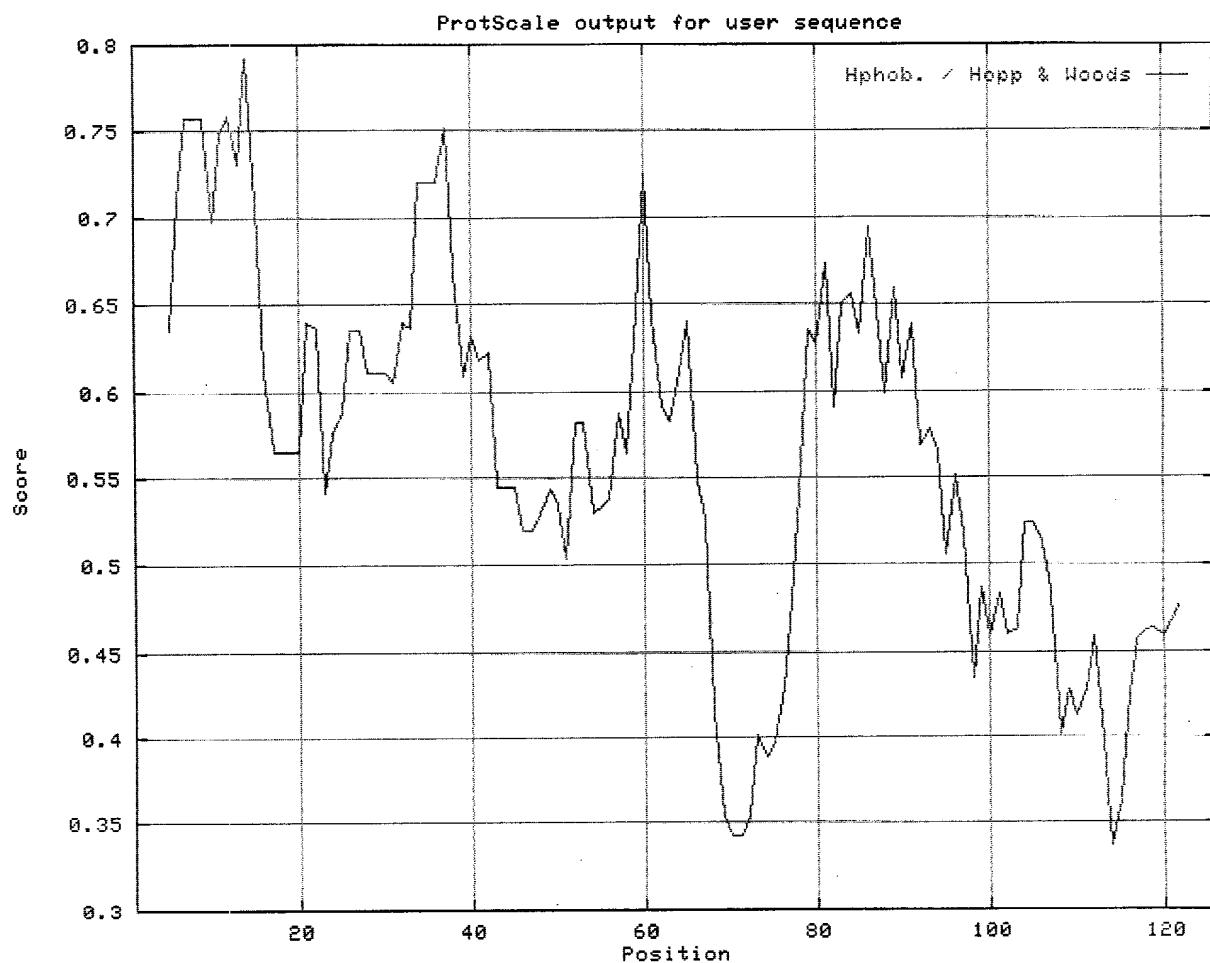


Figure 6A
121P1F1 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

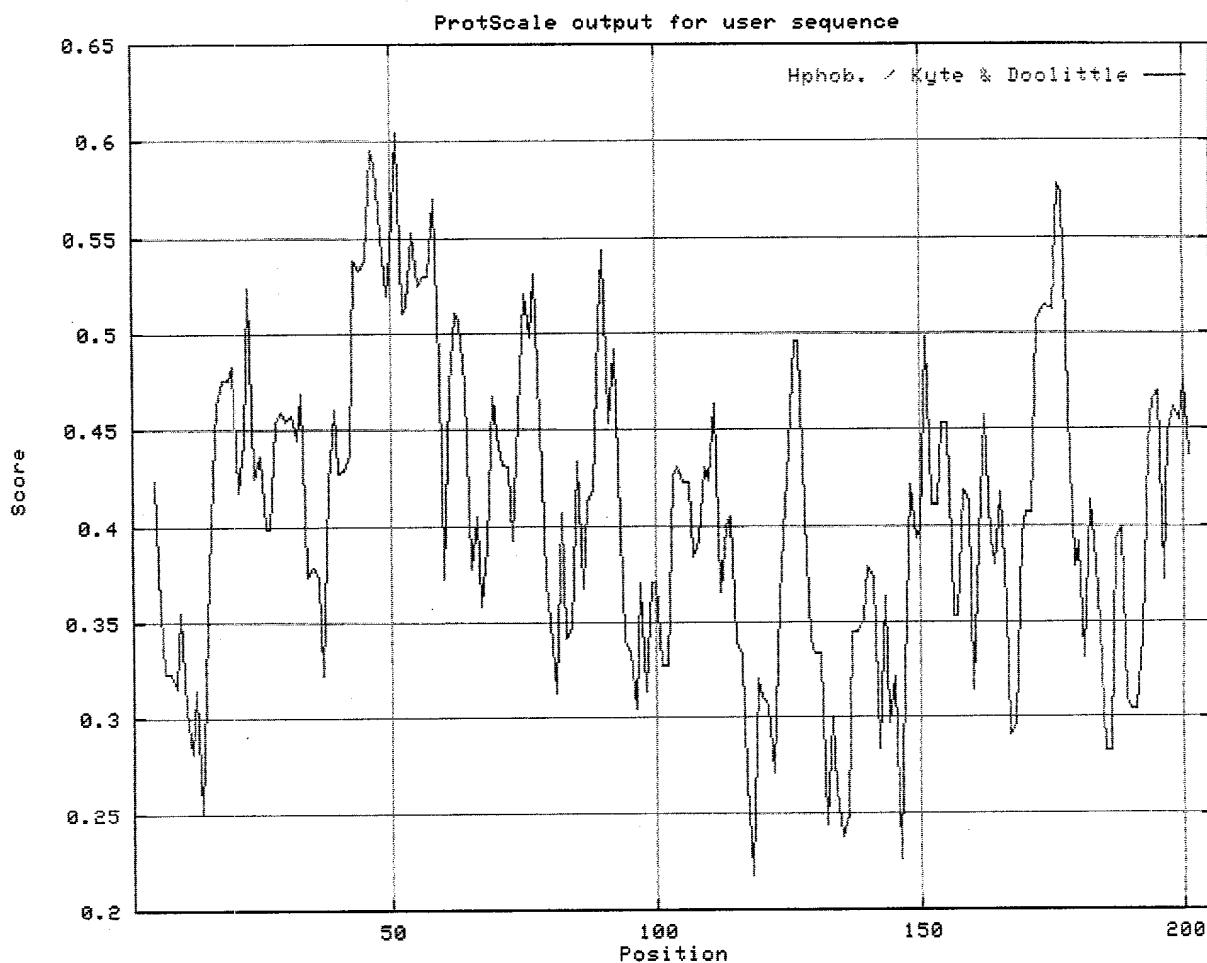


Figure 6B
121P1F1 variant 1a Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

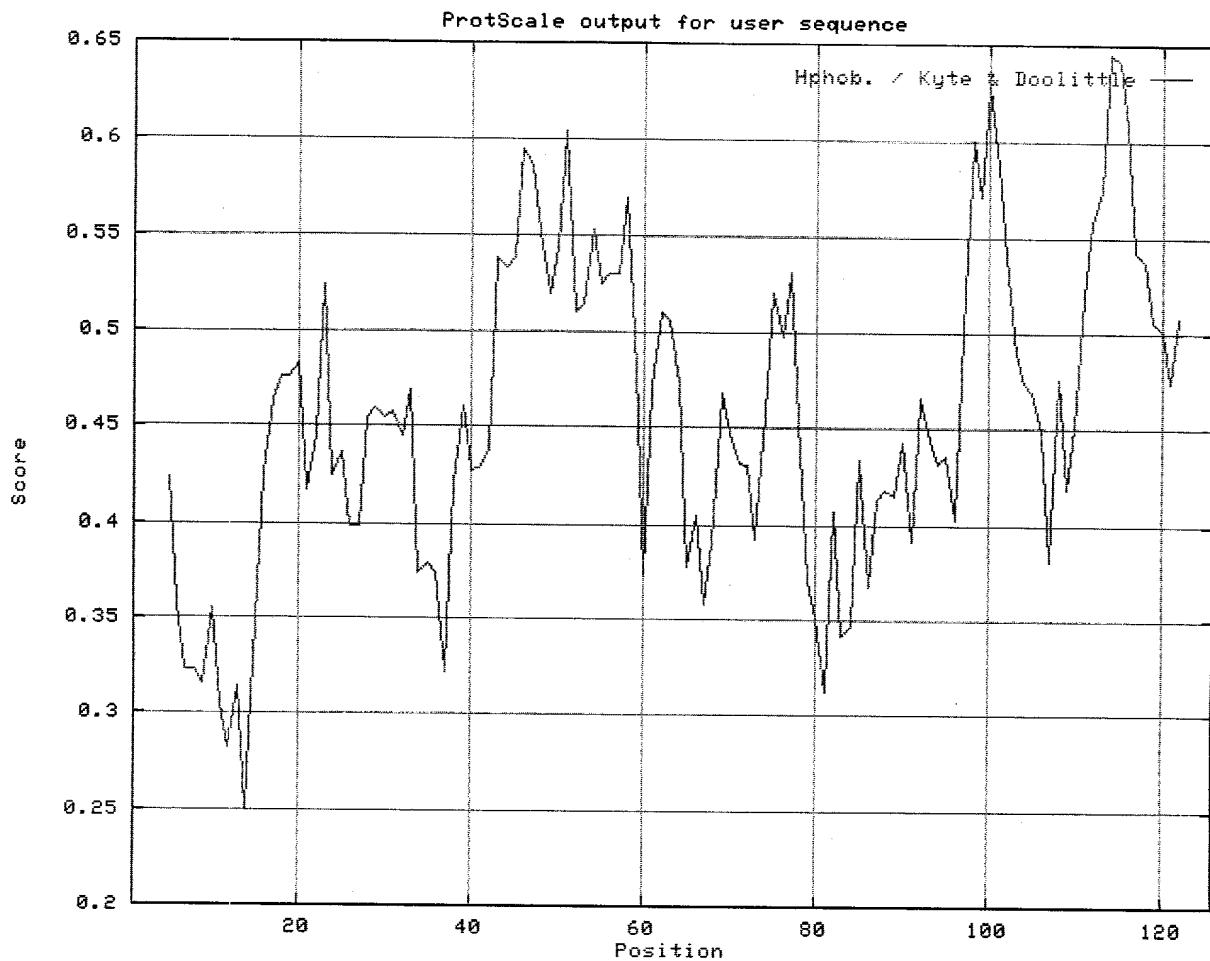


Figure 7A
121P1F1 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

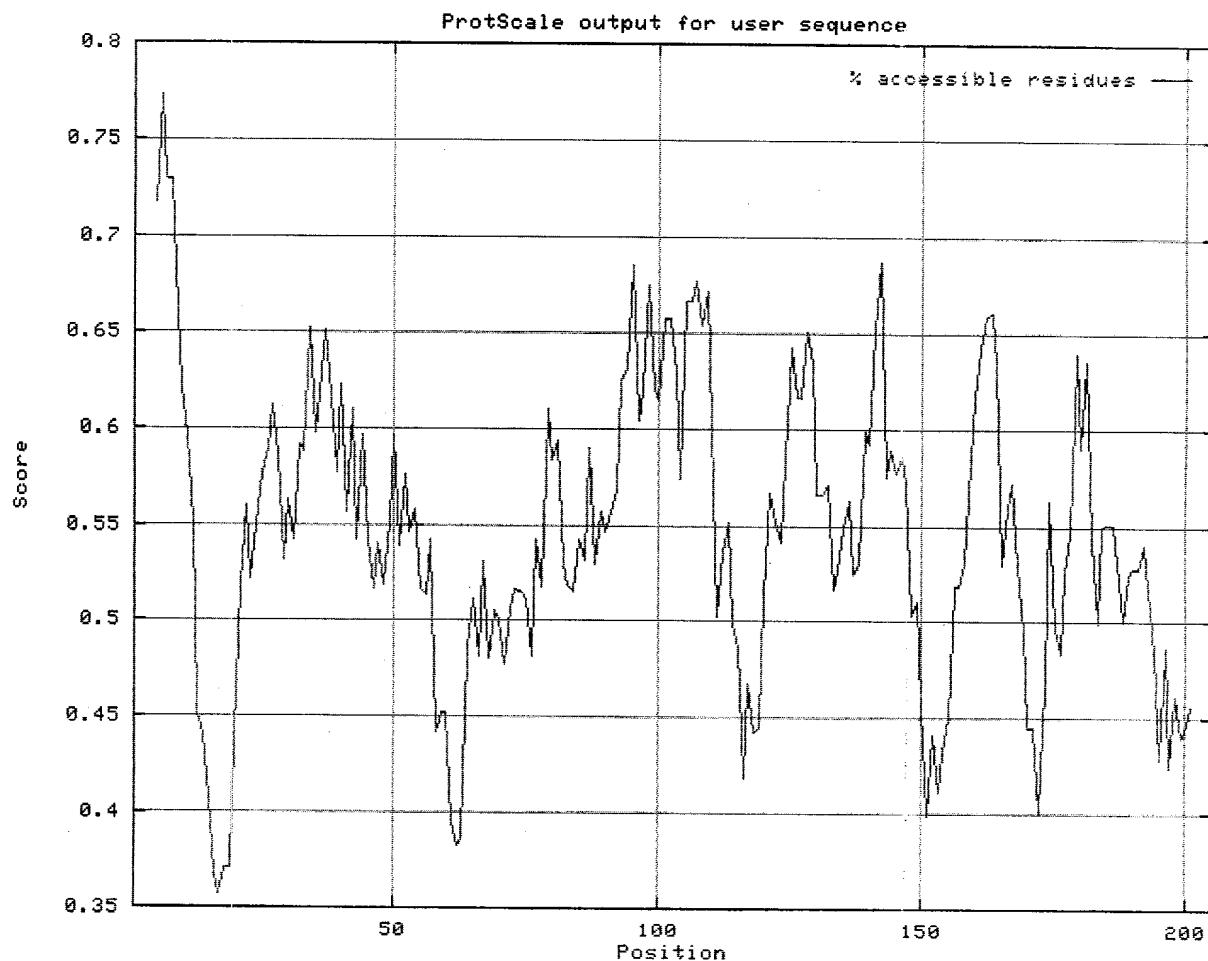


Figure 7B
121P1F1 variant 1a % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

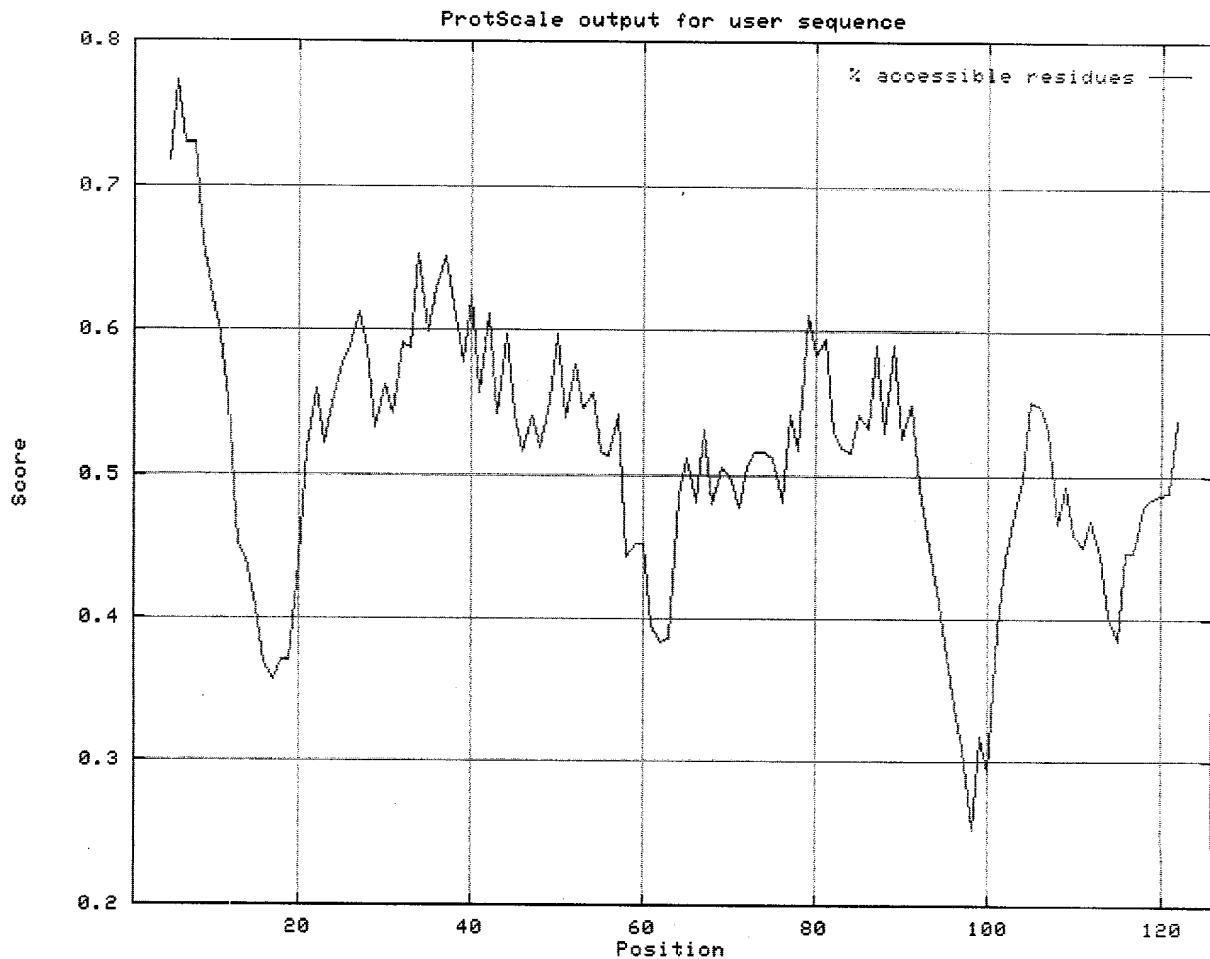


Figure 8A
121P1F1 Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

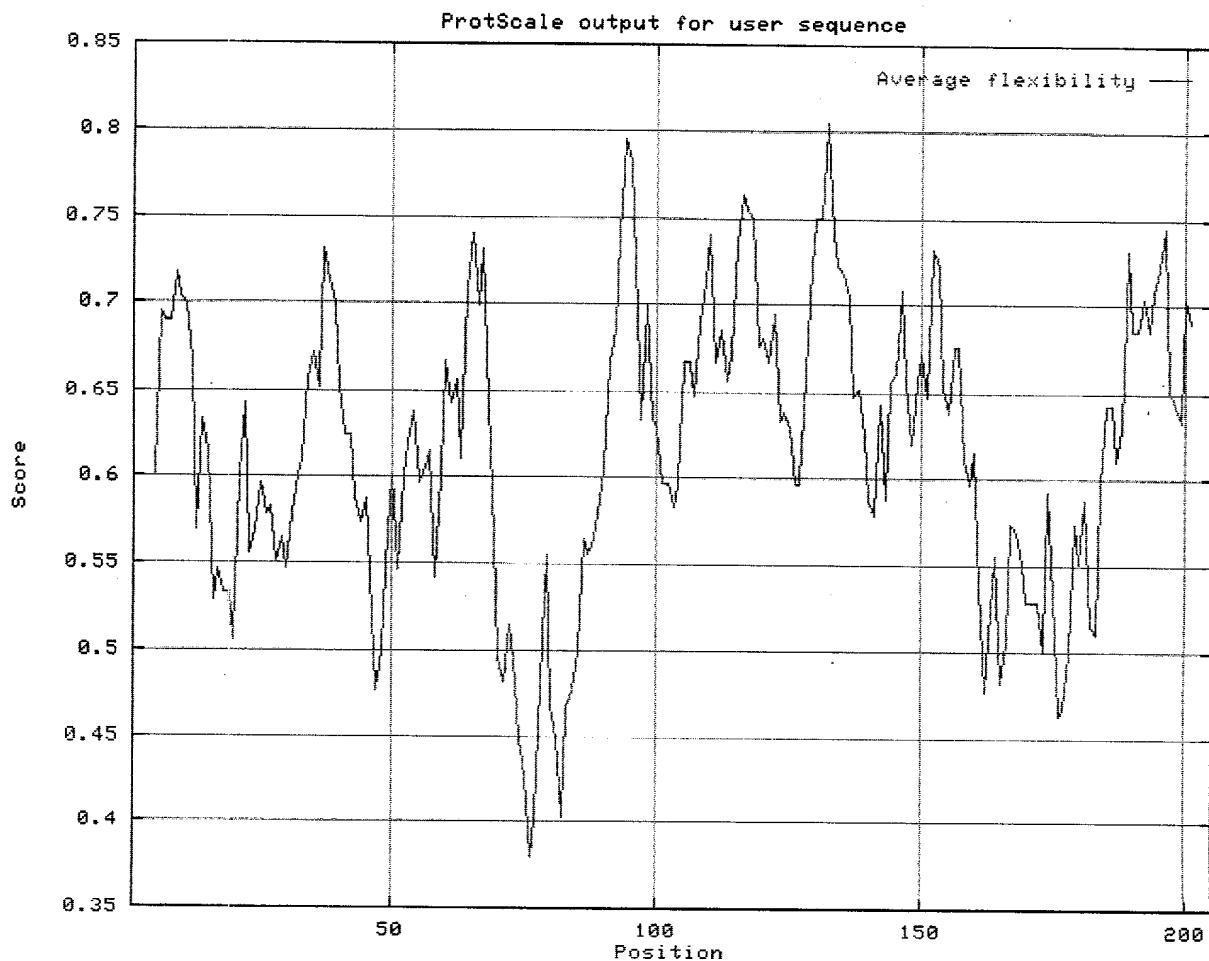


Figure 8B
121P1F1 variant 1a Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

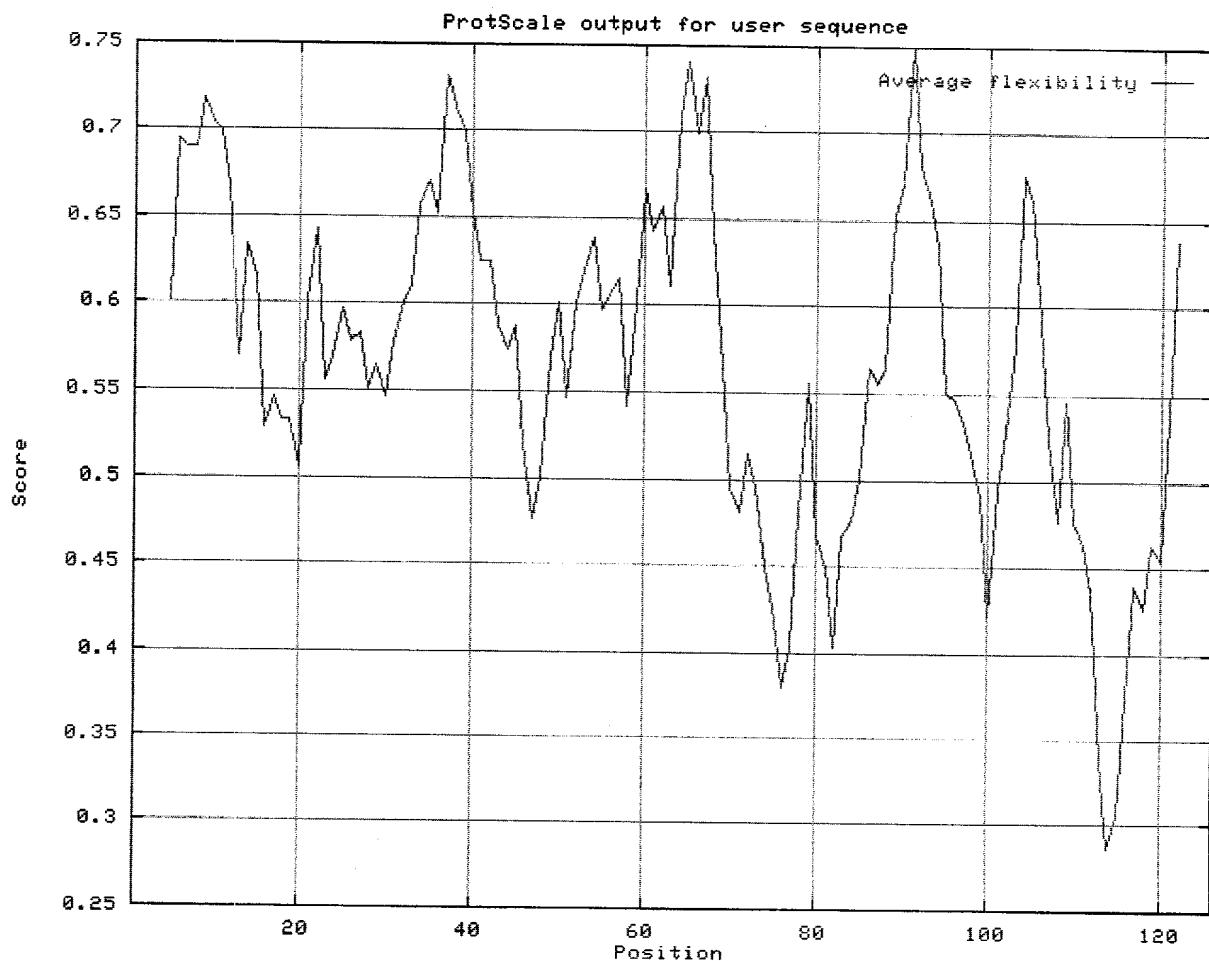


Figure 9A
121P1F1 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

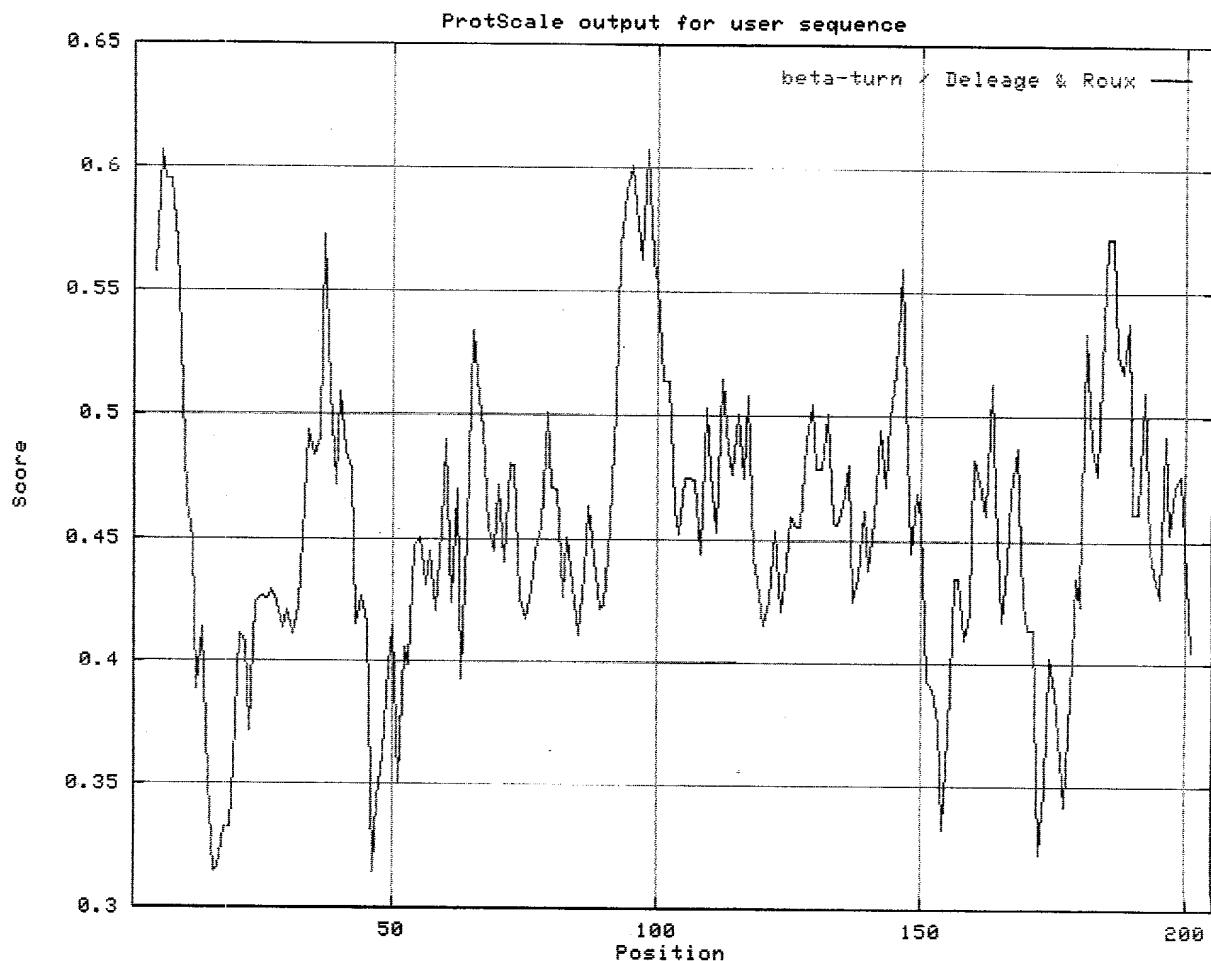


Figure 9B
121P1F1 variant 1a Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

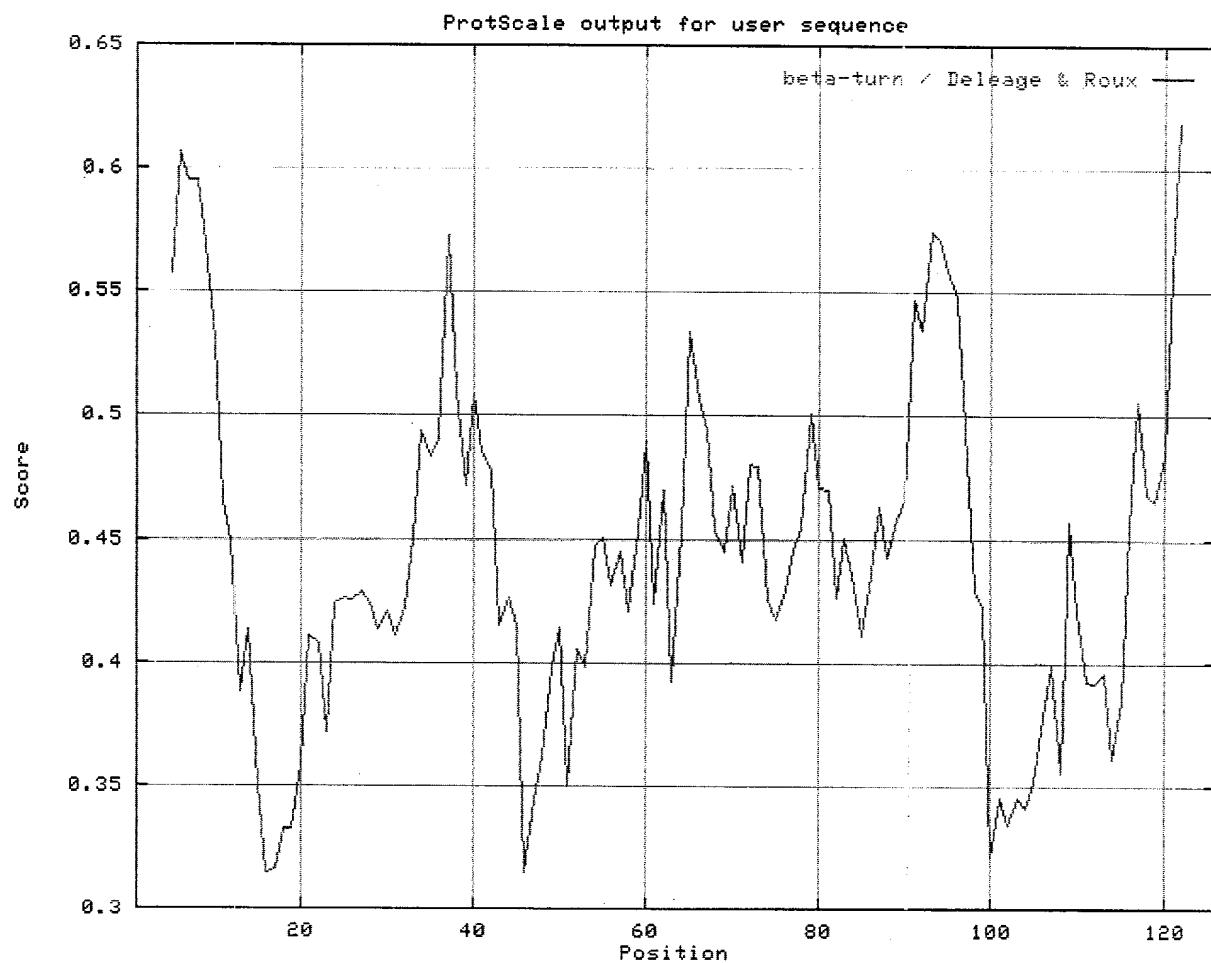
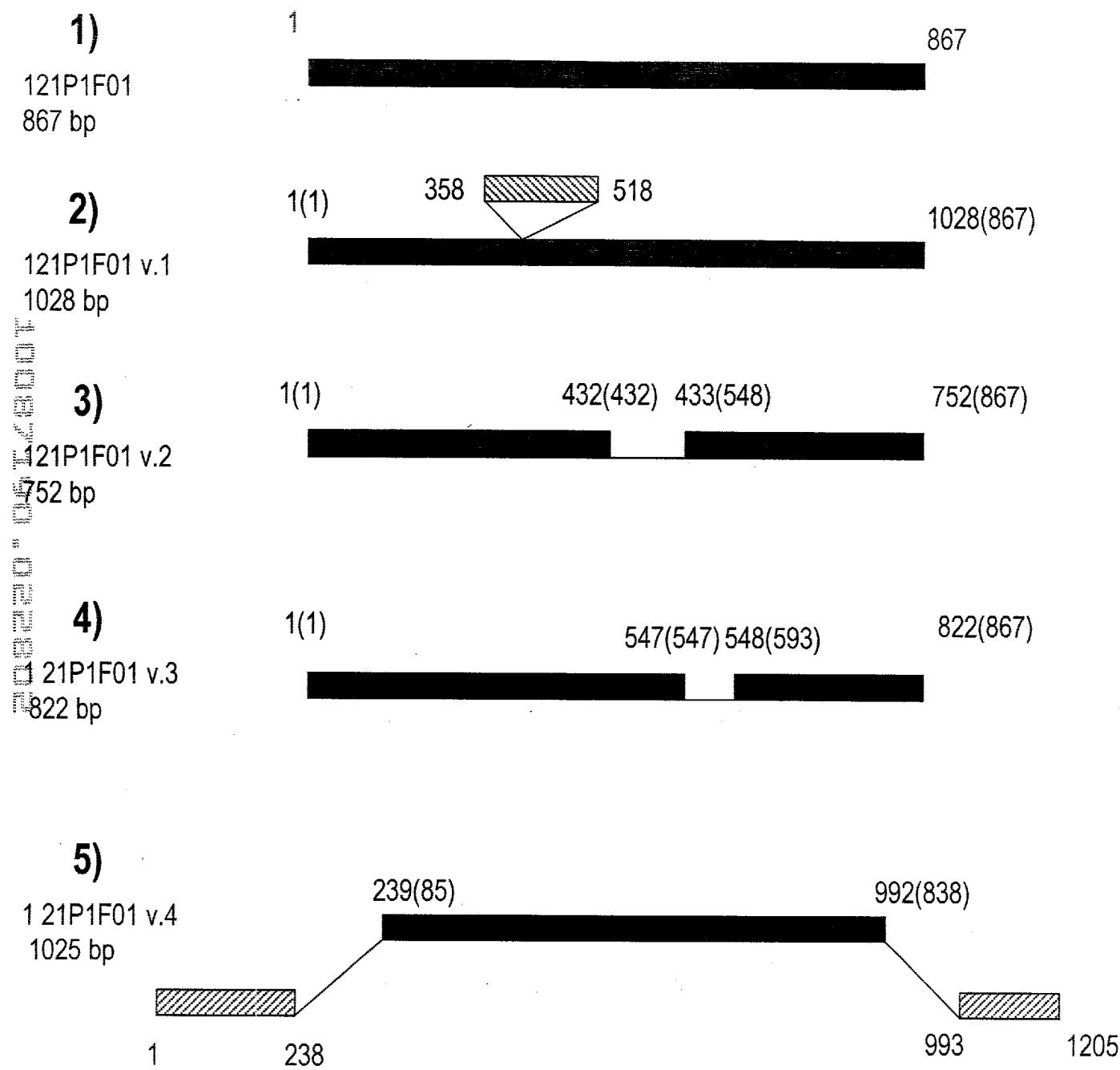
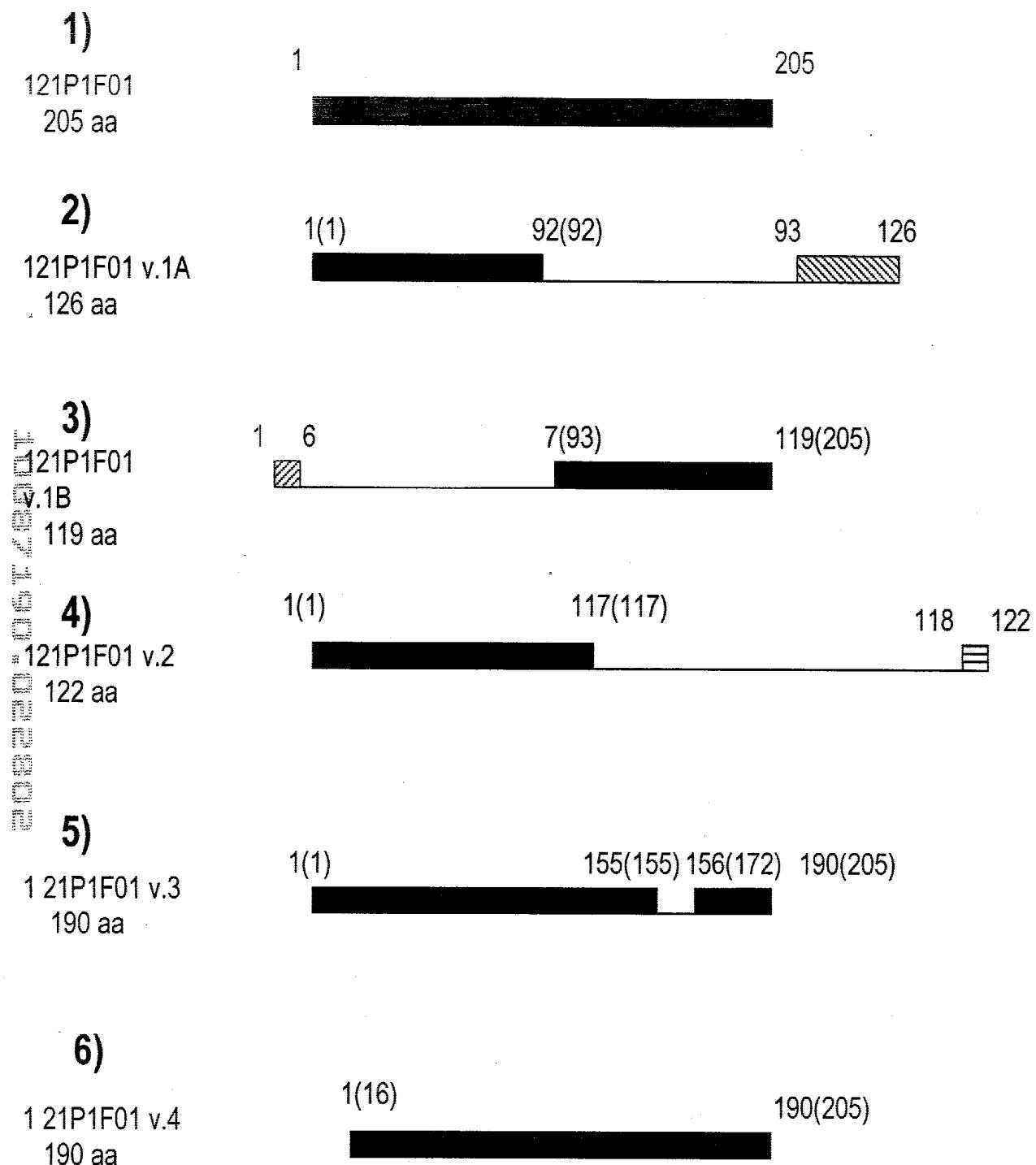


Figure 10



Note: Numbers in "(" correspond to those of the original sequence. Black box shows the same sequence as the original one. SNPs are indicated above the box.

Figure 11



Note: Numbers in "(" correspond to those of the original sequence. Black box shows the same sequence as the original one. Single amino acid variations are indicated above the box.

Figure 12

Specific recognition of 121P1F1 antigen by anti-121P1F1 pAb

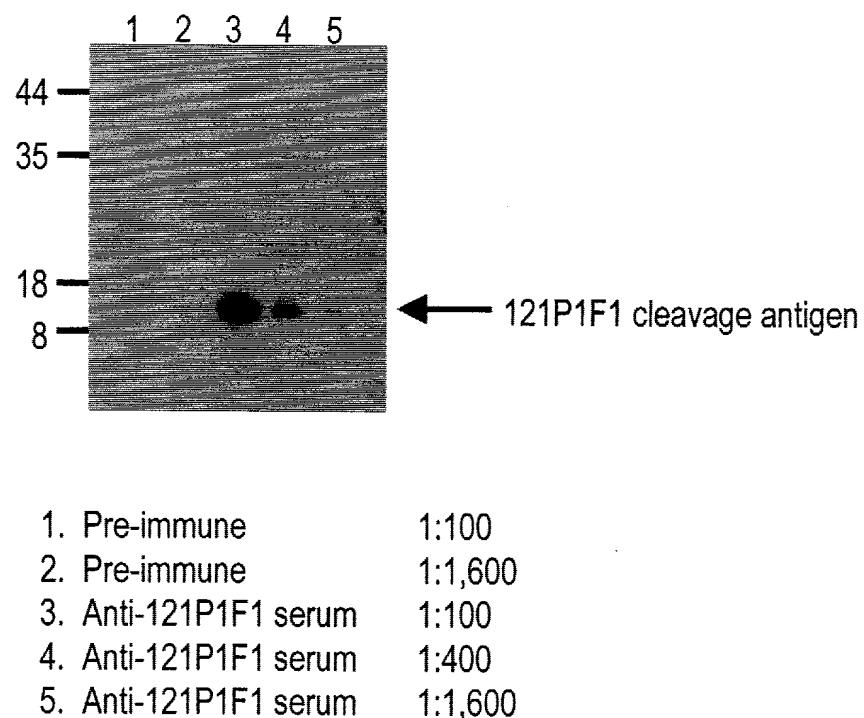


Figure 13
Expression of 121P1F1 in various cancer cells

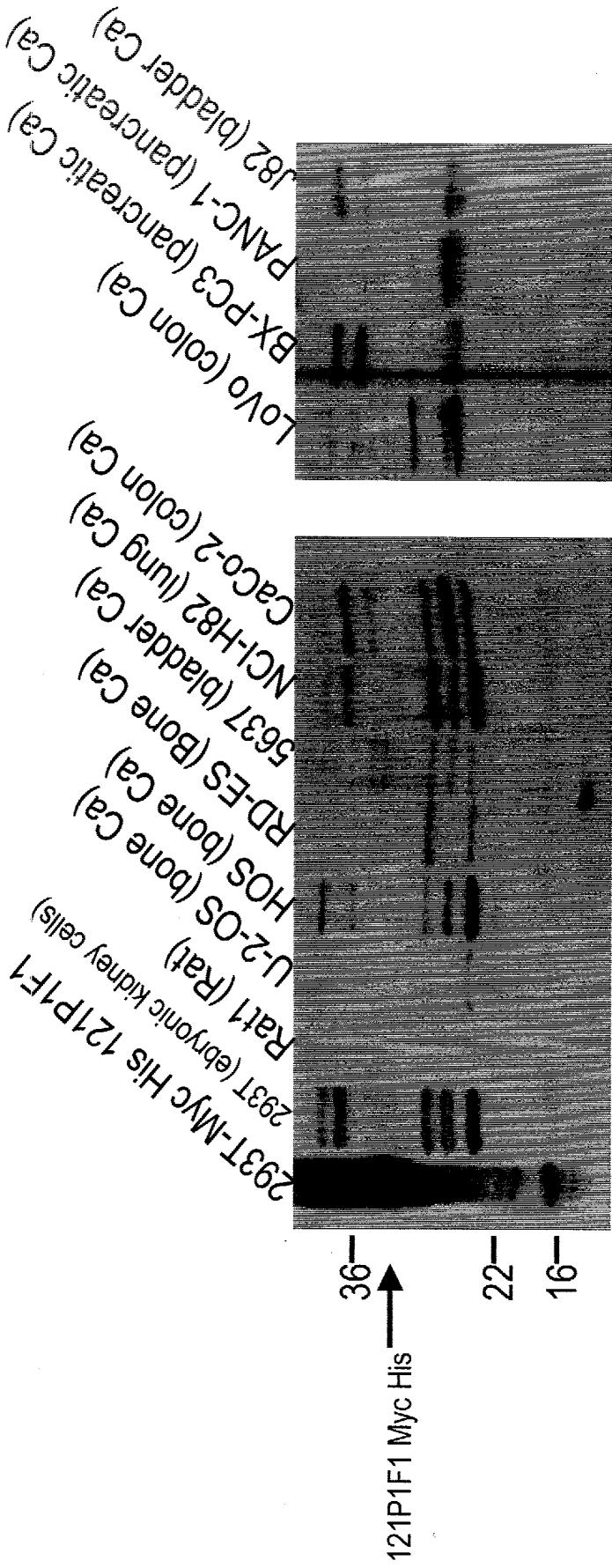


Figure 14 Expression of epitope tagged 121P1F1 in 293T cells

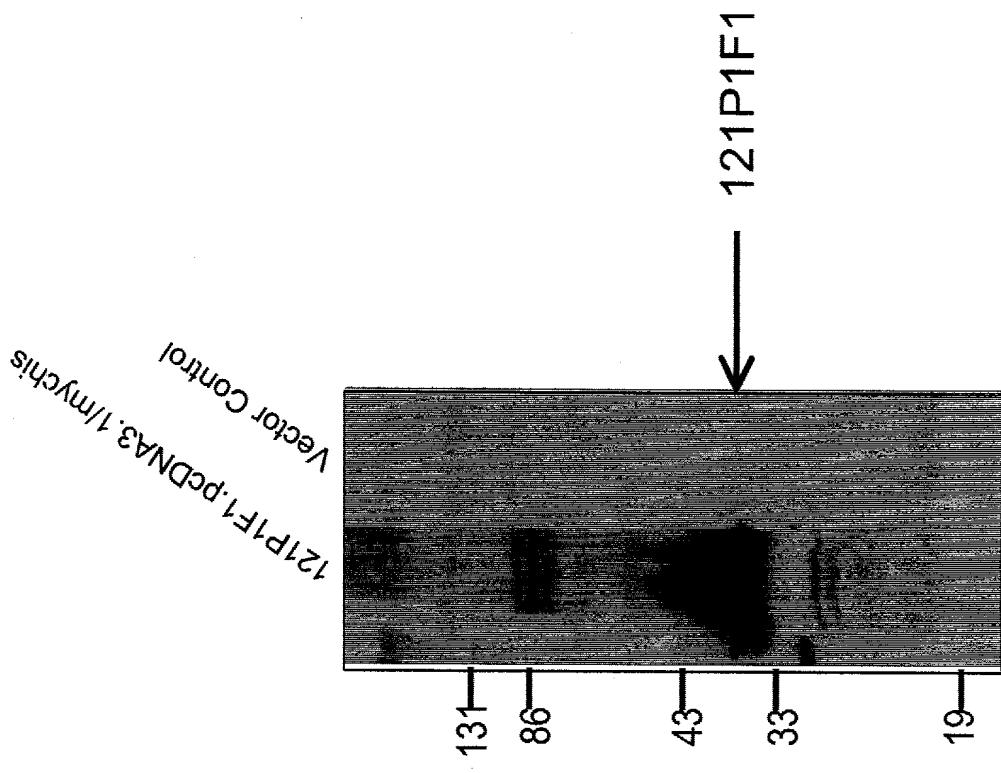


Figure 15 121P1F1 Androgen Regulation *In Vivo*

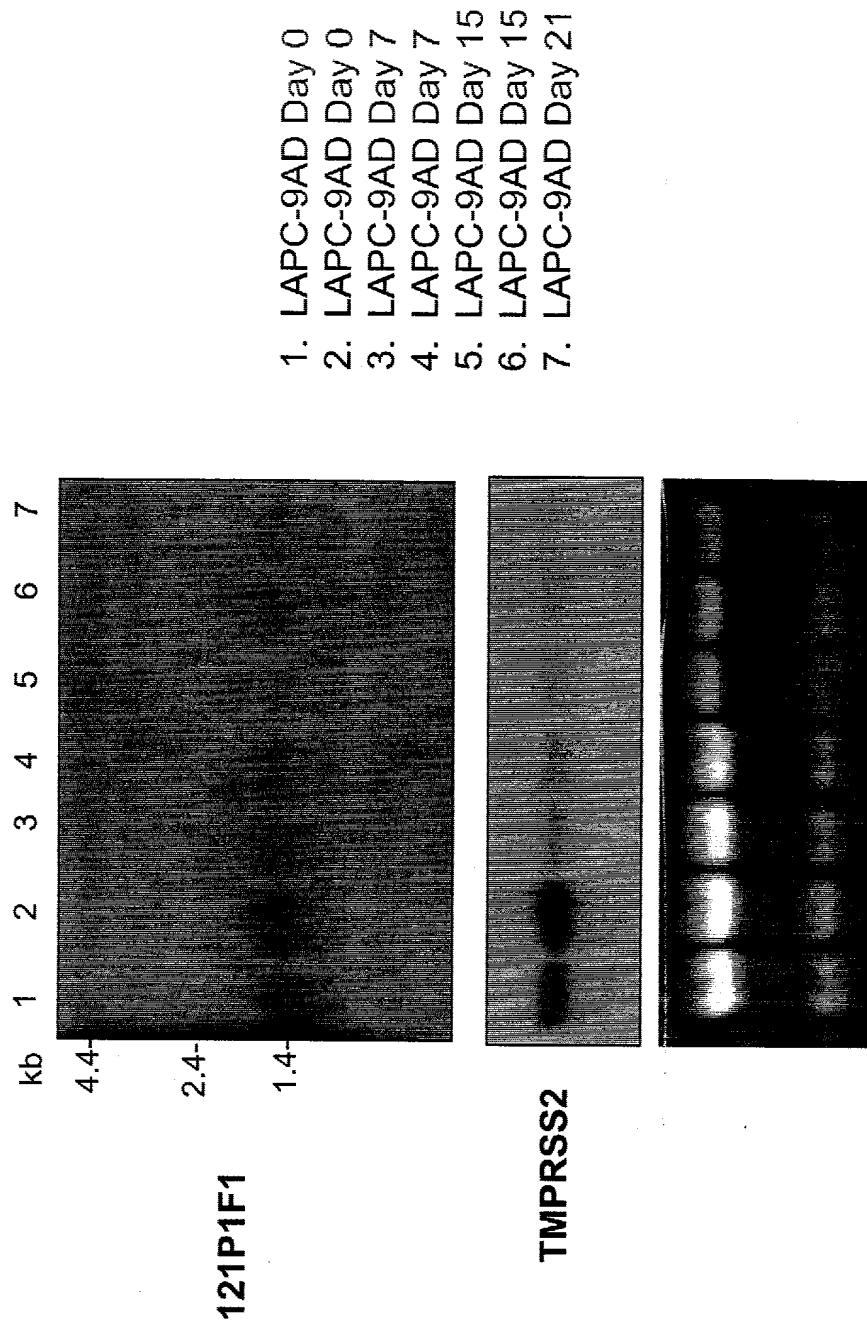


Figure 16A

Secondary structure prediction of 121P1F1

Alpha helix (h) : 61.95% Extended strand (e) : 1.95% Random coil (c) : 36.10%

Figure 16B

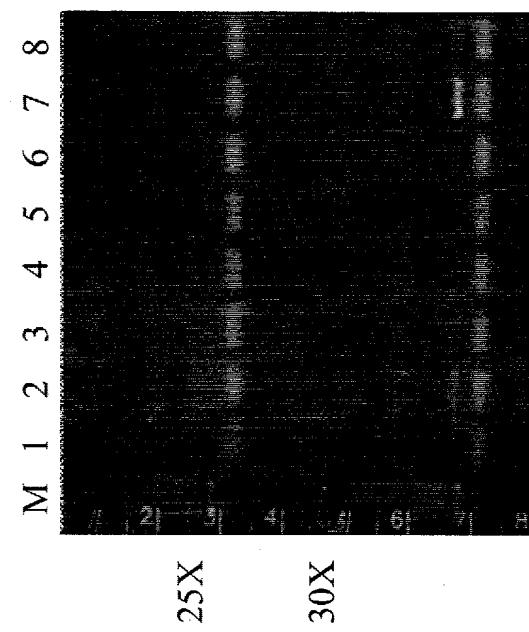
Secondary structure prediction of variant 1a

10 20 30 40 50 60 70
| | | | | | |
MSKKKGLSAEEKRTTRMMEIFSETKDVFQLKDLIKEKIAPEKEKGITAMSVKEVVLQSLIVDDGMVDCERIGTSNY
ccccccchhhhhhhhhhhhhhhhhhhcc
YWAFPSKALHARKHKLLEVLESQDPGCCFHEILIKVSYRKFWLGAVALAHACNPSTLGG
eeeeccchhhcc

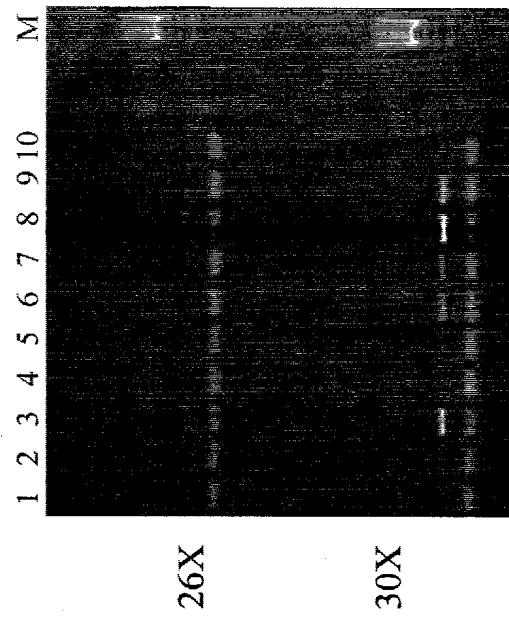
Alpha helix (h) : 50.79% Extended strand (e) : 7.94% Random coil (c) : 41.27%

Figure 17 Expression of 121P1F1 by RT-PCR

A. Human normal tissues



B. Patient tumor specimens



- 1) VP1
- 2) VP2
- 3) XP
- 4) Normal prostate
- 5) Small Int.
- 6) Bladder cancer pool
- 7) Kidney cancer pool
- 8) Colon cancer pool
- 9) Lung tumor
- 10) H2O
- 1) Colon
- 2) Ovary
- 3) Leuk.
- 4) Prost.
- 5) Spleen
- 6) Thymus
- 7) Testis

Figure 18 Expression of 121P1F1 in normal human tissues

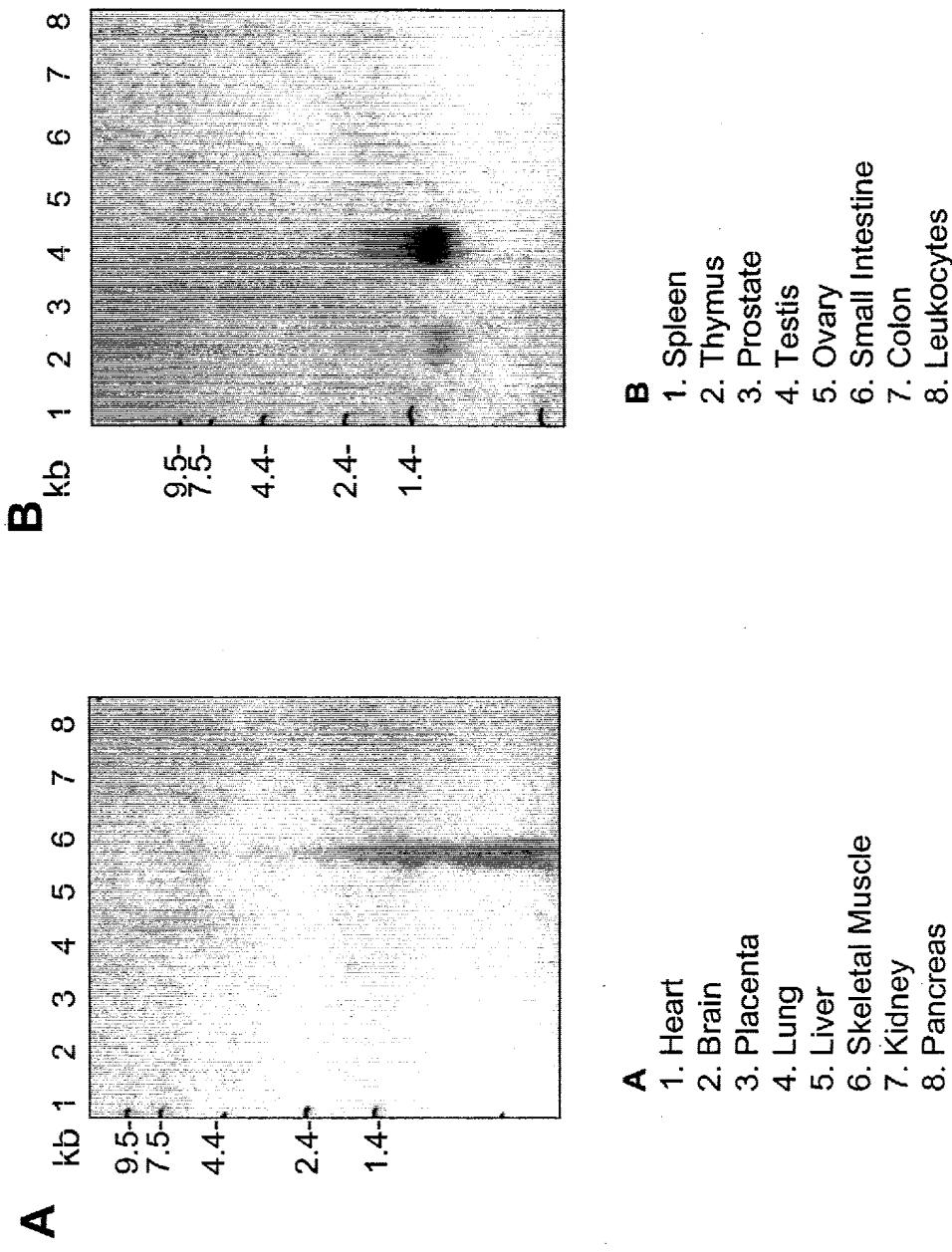


Figure 19 Expression of 121P1F1 in Multiple Cancer Cell lines

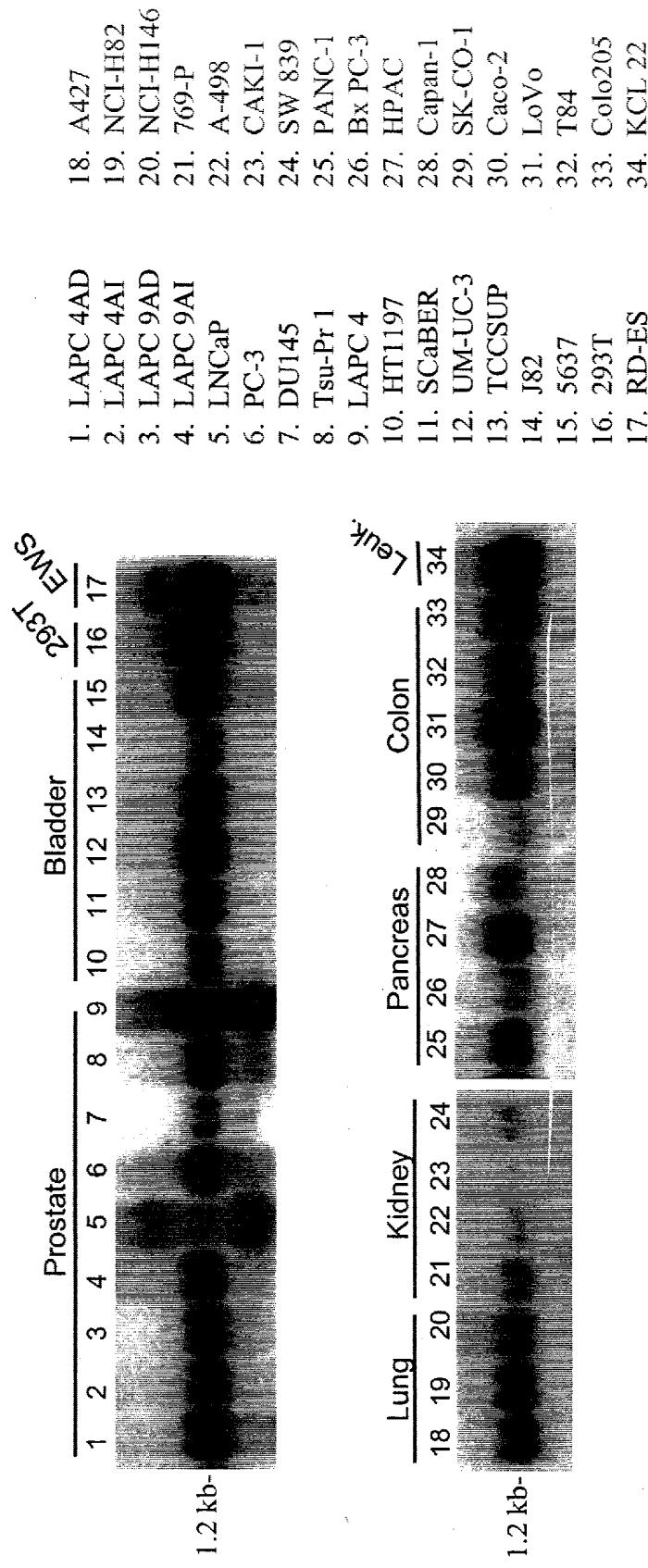


Figure 20 Expression of 121P1F1 in Patient Prostate Cancer Samples

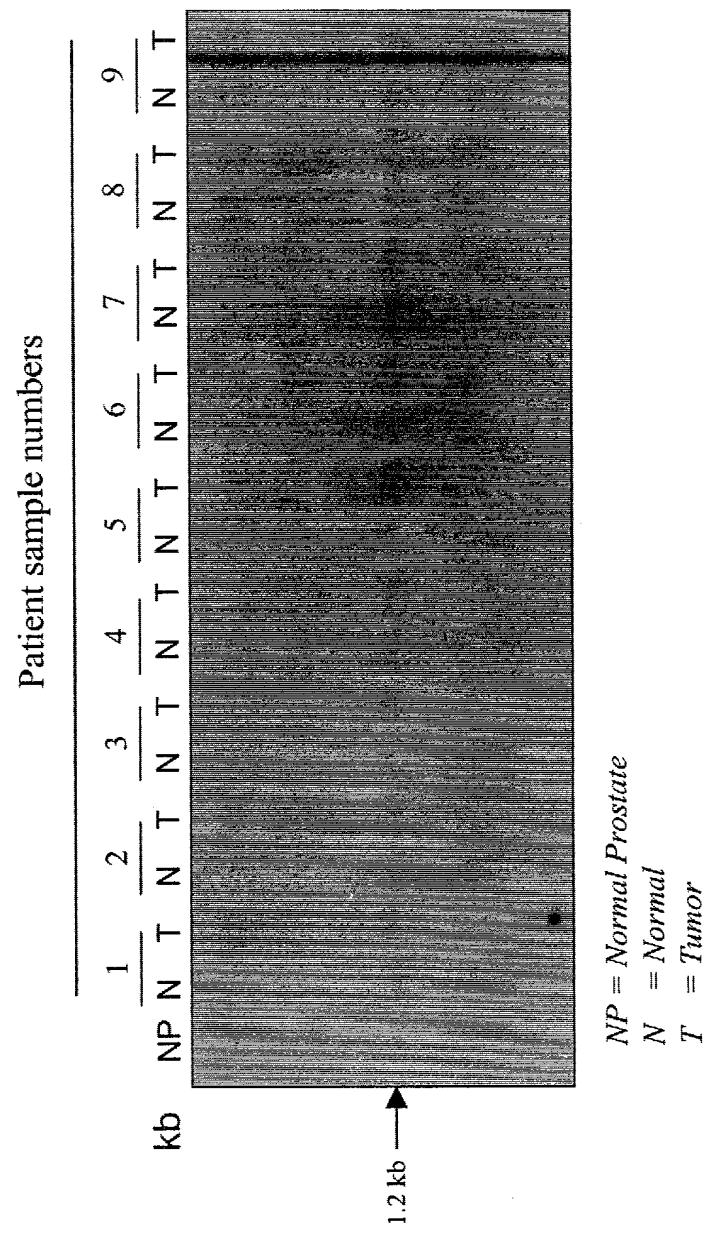
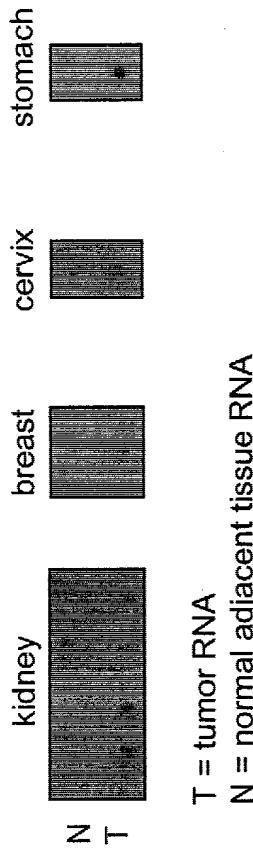


Figure 21 Expression of 121P1F1 in Kidney, Breast, Cervical and Stomach Patients Samples as well as Cancer Cell lines



T = tumor RNA
N = normal adjacent tissue RNA

Cancer cell lines are:
(from left to right)

HeLa (cervical carcinoma)
Daudi (Burkitt's lymphoma)
K562 (CML)
HL-60 (PML)
G361 (melanoma)
A549 (lung carcinoma)
MOLT-4 (lymphoblastic leuk.)
SW480 (colorectal carcinoma)
Raji (Burkitt's lymphoma)



Figure 22 Androgen Regulation of 121P1F1

